

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 13, 2003, 21:41:37 ; Search time 1093 Seconds
(without alignments)
3488.076 Million cell updates/sec

Title: US-09-661-658B-2

Perfect score: 131
Sequence: 1 gcctagataagtgactt.....atgcctaacgactatccctt 131

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_da:*

2: gb_hlg:*

3: gb_in:*

4: gb_cm:*

5: gb_ov:*

6: gb_pat:*

7: gb_pl:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_da:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_of:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_hlg_hum:*

31: em_hlg_inv:*

32: em_hlg_other:*

33: em_hlg_mus:*

34: em_hlg_pln:*

35: em_hlg_rtd:*

36: em_hlg_mam:*

37: em_hlg_vtl:*

38: em_sy:*

39: em_hlg_hum:*

40: em_hlg_mus:*

41: em_hlg_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	131	100.0	131	6	AX379337	AX379337 Sequence
2	127.4	97.3	131	6	AX379340	AX379340 Sequence
3	127.4	97.3	131	6	AX427105	AX427105 Sequence
4	123	93.9	128	6	AX427121	AX427121 Sequence
5	119	90.8	130	6	AX427102	AX427102 Sequence
6	109	83.2	133	6	AX427122	AX427122 Sequence
7	107	81.7	129	6	AX427124	AX427124 Sequence
8	87	66.4	119	6	AX427123	AX427123 Sequence
9	86.4	66.0	117	6	AX427126	AX427126 Sequence
10	83.4	63.7	115	6	AX427125	AX427125 Sequence
11	82.2	62.7	112	6	AX427131	AX427131 Sequence
12	81.4	62.1	107	6	AX427129	AX427129 Sequence
13	80.6	61.5	122	6	AX427116	AX427116 Sequence
14	79.8	60.9	107	6	AX427130	AX427130 Sequence
15	78.4	59.8	126	7	AF158101	AF158101 Bacteriophage T
16	78.4	59.8	126	7	AF158101	AF158101 Bacteriophage T
17	78.2	59.7	124	6	AX427132	AX427132 Sequence
18	78.2	59.7	124	6	AX427132	AX427132 Sequence
19	69.2	52.8	97	6	AX427120	AX427120 Sequence
20	49.6	37.9	144	6	AX427127	AX427127 Sequence
21	45.8	35.0	140	6	AX427128	AX427128 Sequence
22	37.2	28.4	59	6	AR209847	AR209847 Sequence
23	37.2	28.4	123	6	AR209841	AR209841 Sequence
24	37.2	28.4	123	6	AR209841	AR209841 Sequence
25	37.2	28.4	123	6	AR209841	AR209841 Sequence
26	37.2	28.4	123	6	AR209841	AR209841 Sequence
27	37.2	28.4	123	6	AR209841	AR209841 Sequence
28	37.2	28.4	123	6	AR209841	AR209841 Sequence
29	37.2	28.4	123	6	AR209841	AR209841 Sequence
30	34.6	26.4	137	2	AC125856	AC125856 Rattus no
31	34.4	26.3	216	3	AC095703	AC095703 Rattus no
32	34.4	26.3	216	3	AC095703	AC095703 Rattus no
33	33.6	25.6	950	9	AC010406	AC010406 Homo sapi
34	33.6	25.6	183	9	AC010423	AC010423 Homo sapi
35	33	25.2	282	6	AX034873	AX034873 Sequence
36	32.8	25.0	109	2	AC130165	AC130165 Rattus no
37	32.6	24.9	244	6	AX034878	AX034878 Sequence
38	32.6	24.9	283	6	AX034869	AX034869 Sequence
39	32.2	24.6	607	6	AX034876	AX034876 Sequence
40	31.8	24.3	40	6	AX034867	AX034867 Sequence
41	31.8	24.3	42	6	130279	130279 Sequence
42	31.8	24.3	45	6	AX034890	AX034890 Sequence
43	31.8	24.3	256	5	AX034882	AX034882 Sequence
44	31.8	24.3	608	5	AX034875	AX034875 Sequence
45	31.8	24.3	189	2	AC119104	AC119104 Rattus no

ALIGNMENTS

RESULT 1
AX379337
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AX379337
Sequence 2 from Patent WO0196541.
AX379337
GI:19575177
synthetic construct.
synthetic construct.
artificial sequences.
Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M.,
Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.
Allosterically regulated ribozymes
Patent: WO 0196541-A 2 20-DEC-2001;

Db 126 CTT 128

RESULT 5
AX427102 130 bp DNA linear PAT 18-JUN-2002

LOCUS Sequence 2 from Patent WO0196559.

DEFINITION AX427102

ACCESSION AX427102.1 GI:21530485

VERSION

KEYWORDS synthetic construct.

SOURCE synthetic construct.

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Ellington, A.D., Hesselberth, J., Marshall, K., Robertson, M.,

Soeter, L., Davidson, E., Cox, J.C. and Reidel, T.

TITLE Regulatable, catalytically active nucleic acids

JOURNAL Patent: WO 0196559-A 2 20-DEC-2001;

Board of Regents, The University of Texas System (US)

FEATURES

1.130

Location/Qualifiers

source

BASE COUNT 37 a 32 c 24 g 37 t

ORIGIN

Query Match 90.8%; Score 119; DB 6; Length 130;

Best Local Similarity 99.2%; Pred. No. 1.2e-29;

Matches 130; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1 GCCCTGAGTATAGGCTGCTATCTGATCTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60

1 GCCCTGAGTATAGGCTGCTATCTGATCTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60

61 CAATCCGCTGCTAAATTAATACAGATCGCTGATGCGCCCTGGCAGATTAATGCTTAAC 120

61 CAATCCGCTGCTAAATTAATACAGATCGCTGATGCGCCCTGGCAGATTAATGCTTAAC 119

121 GACTATCCCTT 131

120 GACTATCCCTT 130

Db

RESULT 6

AX427122 133 bp DNA linear PAT 18-JUN-2002

LOCUS Sequence 22 from Patent WO0196559.

DEFINITION AX427122

ACCESSION AX427122.1 GI:21530505

VERSION

KEYWORDS synthetic construct.

SOURCE synthetic construct.

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Ellington, A.D., Hesselberth, J., Marshall, K., Robertson, M.,

Soeter, L., Davidson, E., Cox, J.C. and Reidel, T.

TITLE Regulatable, catalytically active nucleic acids

JOURNAL Patent: WO 0196559-A 2 20-DEC-2001;

Board of Regents, The University of Texas System (US)

FEATURES

1.133

Location/Qualifiers

source

BASE COUNT 37 a 33 c 25 g 38 t

ORIGIN

Query Match 83.2%; Score 109; DB 6; Length 133;

Best Local Similarity 98.5%; Pred. No. 2.9e-26;

Matches 131; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

1 GCCCTGAGTATAGGCTGCTATCTGATCTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60

Db

1 GCCCTGAGTATAGGCTGCTATCTGATCTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60

61 CAATCCGCTGCTAAATTAATACAGATCGCTGATGCGCCCTGGCAGATTAATGCTTAAC 118

61 CAATCCGCTGCTAAATTAATACAGATCGCTGATGCGCCCTGGCAGATTAATGCTTAAC 120

119 ACGATATCCCTT 131

121 ACGATATCCCTT 133

Db

RESULT 7

AX427124 129 bp DNA linear PAT 18-JUN-2002

LOCUS Sequence 24 from Patent WO0196559.

DEFINITION AX427124

ACCESSION AX427124.1 GI:21530507

VERSION

KEYWORDS synthetic construct.

SOURCE synthetic construct.

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Ellington, A.D., Hesselberth, J., Marshall, K., Robertson, M.,

Soeter, L., Davidson, E., Cox, J.C. and Reidel, T.

TITLE Regulatable, catalytically active nucleic acids

JOURNAL Patent: WO 0196559-A 24 20-DEC-2001;

Board of Regents, The University of Texas System (US)

FEATURES

1.129

Location/Qualifiers

source

BASE COUNT 36 a 32 c 24 g 37 t

ORIGIN

Query Match 81.7%; Score 107; DB 6; Length 129;

Best Local Similarity 98.5%; Pred. No. 1.4e-25;

Matches 129; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

1 GCCCTGAGTATAGGCTGCTATCTGATCTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60

1 GCCCTGAGTATAGGCTGCTATCTGATCTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60

61 CAATCCGCTGCTAAATTAATACAGATCGCTGATGCGCCCTGGCAGATTAATGCTTAAC 120

61 CAATCCGCTGCTAAATTAATACAGATCGCTGATGCGCCCTGGCAGATTAATGCTTAAC 118

121 GACTATCCCTT 131

119 GACTATCCCTT 129

Db

RESULT 8

AX427123 119 bp DNA linear PAT 18-JUN-2002

LOCUS Sequence 23 from Patent WO0196559.

DEFINITION AX427123

ACCESSION AX427123.1 GI:21530506

VERSION

KEYWORDS synthetic construct.

SOURCE synthetic construct.

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Ellington, A.D., Hesselberth, J., Marshall, K., Robertson, M.,

Soeter, L., Davidson, E., Cox, J.C. and Reidel, T.

TITLE Regulatable, catalytically active nucleic acids

JOURNAL Patent: WO 0196559-A 23 20-DEC-2001;

Board of Regents, The University of Texas System (US)

FEATURES

1.119

Location/Qualifiers

source

BASE COUNT 37 a 33 c 25 g 38 t

ORIGIN

Query Match 83.2%; Score 109; DB 6; Length 133;

Best Local Similarity 98.5%; Pred. No. 2.9e-26;

Matches 131; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

1 GCCCTGAGTATAGGCTGCTATCTGATCTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60


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REFERENCE
AUTHORS      1
              Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M.,
              Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.
TITLE
JOURNAL      Regulatable, catalytically active nucleic acids
              Patent: WO 0196559-A 29 20-DEC-2001;
              Board of Regents, The University of Texas System (US)
FEATURES
SOURCE
              1. 107
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="Oligonucleotide"
BASE COUNT   31 a      28 c      19 g      29 t
ORIGIN
Query Match  62.1%; Score 81.4; DB 6; Length 107;
Best Local Similarity 97.2%; Pred. No. 6,6e-17;
Matches 104; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 27 GTAATCTATCTAAAGGGGAACTCTCTAGTACAAATCCGCTAAATT-ATACCAGC 85
    |||||||
Db 1 GTAATCTATCTAAAGGGGAACTCTCTCTAGTACAAATCCGCTAAATTATACACAGC 60
    |||||||

QY 86 ATCGCTTGATGCCCTTGGCAG-ATAAATGCCCTTAACGACTATCCCTT 131
    |||||||
Db 61 ATCGCTTGATGCCCTTGGCAGATAAATGCCCTTAACGACTATCCCTT 107
    |||||||

RESULT 13
AX427116      122 bp      DNA      linear      PAT 18-JUN-2002
LOCUS
DEFINITION   Sequence 16 from Patent WO0196559.
ACCESSION    AX427116
VERSION      AX427116.1 GI:21530499
KEYWORDS
SOURCE       synthetic construct.
ORGANISM     synthetic construct
              artificial sequences.
REFERENCE
AUTHORS      1
              Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M.,
              Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.
TITLE
JOURNAL      Regulatable, catalytically active nucleic acids
              Patent: WO 0196559-A 16 20-DEC-2001;
              Board of Regents, The University of Texas System (US)
FEATURES
SOURCE       1. 122
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="Oligonucleotide"
BASE COUNT   34 a      29 c      24 g      35 t
ORIGIN
Query Match  61.5%; Score 80.6; DB 6; Length 122;
Best Local Similarity 82.4%; Pred. No. 1.2e-16;
Matches 108; Conservative 0; Mismatches 14; Indels 9; Gaps 1;

QY 1 GCCGTAGTATAGGTGACTTATCTATCTATCTATCTAAAGGGGAACTCTCTAGTAGA 60
    |||||||
Db 1 GCCGTAGTATAGGTGACTTATCTATCTATCTATCTAAAGGGGAACTCTCTAGTAGA 60
    |||||||

QY 61 CAATCCCGTCTAAATTATACAGCATCGTCTTGATGCCCTTGGCAGATTAATGCCCTAAC 120
    |||||||
Db 61 CAATCCCGTCTAAATTATAGAGACTGCC-----CGGGTCTTACATTAATGAAGCTTAAC 111
    |||||||

QY 121 GACTATGCCCTT 131
    |||||||
Db 112 GACTATGCCCTT 122
    |||||||

RESULT 14
AX427130      107 bp      DNA      linear      PAT 18-JUN-2002
LOCUS
DEFINITION   Sequence 30 from Patent WO0196559.
ACCESSION    AX427130

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VERSION      AX427130.1 GI:21530513
KEYWORDS
SOURCE       synthetic construct.
ORGANISM     synthetic construct
              artificial sequences.
REFERENCE
AUTHORS      1
              Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M.,
              Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.
TITLE
JOURNAL      Regulatable, catalytically active nucleic acids
              Patent: WO 0196559-A 30 20-DEC-2001;
              Board of Regents, The University of Texas System (US)
FEATURES
SOURCE       1. 107
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="Oligonucleotide"
BASE COUNT   29 a      28 c      19 g      31 t
ORIGIN
Query Match  60.9%; Score 79.8; DB 6; Length 107;
Best Local Similarity 96.3%; Pred. No. 2.3e-16;
Matches 103; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 27 GTAATCTATCTAAAGGGGAACTCTCTAGTACAAATCCGCTAAATT-ATACCAGC 85
    |||||||
Db 1 GTAATCTATCTAAAGGGGAACTCTCTCTAGTACAAATCCGCTAAATTATACACAGC 60
    |||||||

QY 86 ATCGCTTGATGCCCTTGGCAG-ATAAATGCCCTTAACGACTATCCCTT 131
    |||||||
Db 61 ATCGCTTGATGCCCTTGGTGTGCAATAAATGCCCTTAACGACTATCCCTT 107
    |||||||

RESULT 15
AR013973      510 bp      DNA      linear      PAT 05-DEC-1998
LOCUS
DEFINITION   Sequence 1 from patent US 5773244.
ACCESSION    AR013973
VERSION      AR013973.1 GI:3971427
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE
AUTHORS      1 (bases 1 to 510)
              Ares,M. Jr. and Foid,E.E.
TITLE
JOURNAL      Methods of making circular RNA
              Patent: US 5773244-A 1 30-JUN-1998;
              Location/Qualifiers
FEATURES
SOURCE       1. 510
              /organism="unknown"
BASE COUNT   153 a      80 c      109 g      168 t
ORIGIN
Query Match  59.8%; Score 78.4; DB 6; Length 510;
Best Local Similarity 98.8%; Pred. No. 7.7e-16;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCGTAGTATAGGTGACTTATCTATCTATCTATCTAAAGGGGAACTCTCTAGTAGA 60
    |||||||
Db 341 GCCGTAGTATAGGTGACTTATCTATCTATCTATCTAAAGGGGAACTCTCTAGTAGA 400
    |||||||

QY 61 CAATCCCGTCTAAATTATA 80
    |||||||
Db 401 CAATCCCGTCTAAATTGTA 420
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Search completed: July 13, 2003, 22:53:39
 Job time : 1094 secs

PT assays for detecting the presence of ligands or activation of an effector of RCANA.

XX Example 1; Page 40; 126pp; English.

CC The present invention relates to regulatable, catalytically active nucleic acids (RCNAs) which are regulated by polypeptides. These are useful for regulating gene expression, in assays for detecting the presence of ligands, for activation of an effector of RCANA, and in gene therapy. The present sequence is an oligonucleotide used in the construction of an RCANA.

SO Sequence 131 BP; 37 A; 32 C; 24 G; 38 T; 0 other;

Query Match 100.0%; Score 131; DB 24; Length 131;
Best Local Similarity 100.0%; Pred. No. 5,4e-38;

Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGAGTATAAGGTGACTTATCTGTAATCTAATCAACGGGGAACCTCTCTAGTACA 60
DB 1 GCCTGAGTATAAGGTGACTTATCTGTAATCTAATCAACGGGGAACCTCTCTAGTACA 60

QY 61 CAATCCGCTGCTAATATATACAGCATCGCTGATGCCCTTGCGAGATAATGCCCTAAC 120
DB 61 CAATCCGCTGCTAATATATACAGCATCGCTGATGCCCTTGCGAGATAATGCCCTAAC 120

QY 121 GACTATCCCTT 131
DB 121 GACTATCCCTT 131

RESULT 2

AAL43049 standard; DNA; 131 BP.

AC AAL43049;

DT 25-SEP-2002 (first entry)

DE Regulatable, catalytically active nucleic acid construction oligo #8.

KM Regulatable catalytically active nucleic acid; RCANA; ribozyme;

OS Synthetic.

PN WO200196559-A2.

PD 20-DEC-2001.

PF 14-JUN-2001; 2001WO-US19302.

PR 15-JUN-2000; 2000US-212097P.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;
PI Davidson E, Cox JC, Reidel T;

DR WPI; 2002-122216/16.

PT New regulatable, catalytically active nucleic acids (RCANA), useful in gene therapy (particularly for regulating gene expression), or in assays for detecting the presence of ligands or activation of an effector of RCANA.

XX Example 5; Page 68; 126pp; English.

CC The present invention relates to regulatable, catalytically active nucleic acids (RCNAs) which are regulated by polypeptides. These are useful for regulating gene expression, in assays for detecting the presence of ligands, for activation of an effector of RCANA, and in gene therapy. The present sequence is an oligonucleotide used in the

CC construction of an RCANA.

SO Sequence 131 BP; 37 A; 32 C; 24 G; 38 T; 0 other;

Query Match 100.0%; Score 131; DB 24; Length 131;
Best Local Similarity 100.0%; Pred. No. 5,4e-38;

Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGAGTATAAGGTGACTTATCTGTAATCTAATCAACGGGGAACCTCTCTAGTACA 60
DB 1 GCCTGAGTATAAGGTGACTTATCTGTAATCTAATCAACGGGGAACCTCTCTAGTACA 60

QY 61 CAATCCGCTGCTAATATATACAGCATCGCTGATGCCCTTGCGAGATAATGCCCTAAC 120
DB 61 CAATCCGCTGCTAATATATACAGCATCGCTGATGCCCTTGCGAGATAATGCCCTAAC 120

QY 121 GACTATCCCTT 131
DB 121 GACTATCCCTT 131

RESULT 3

ABN83045 standard; DNA; 131 BP.

AC ABN83045;

DT 16-AUG-2002 (first entry)

DE Aptazyme construct oligonucleotide GpTtHP6.131.

KW Aptazyme; regulatable; aptamer; luciferase; cyclic AMP; GpTtHP6.131; ss.

OS Unidentified.

PN WO200196541-A2.

PD 20-DEC-2001.

PF 15-JUN-2001; 2001WO-US19119.

PR 15-JUN-2000; 2000US-0661658.

PA (TEXA) UNIV TEXAS.

PI Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;
PI Davidson E, Cox JC, Reidel T;

DR WPI; 2002-090203/12.

PT Aptazyme construct for detecting the presence of ligands, comprises a regulatable group I intron aptamer oligonucleotide with a regulatory domain, and modulates their kinetic parameters in response to an effector.

XX Claim 7; Page 30; 42pp; English.

CC The sequence represents an oligonucleotide used in the invention in the construction of a group I regulatable aptazyme. The invention relates to a novel aptazyme construct comprising a regulatable group I intron aptamer oligonucleotide sequence having an allosterically regulatable target gene vary in response to the kinetic parameters of the aptazyme on a molecule with the regulatory domain, and the intron splicing reaction occurs in vitro. The aptazyme is useful: (1) in assays to detect the presence of ligands or to detect activation of an aptazyme by an effector; (2) in the identification, isolation and enhancement of allosteric effectors and of the allosterically regulatable aptazymes with which they interact; (3) to activate or repress a reporter gene (e.g. luciferase) containing an engineered intron in response to an endogenous activator; and (4) to monitor intracellular levels of proteins or small molecules such as cyclic AMP.

Sequence 131 BP; 37 A; 32 C; 24 G; 38 T; 0 other;

Query Match 100.0%; Score 131; DB 24; Length 131;

Best Local Similarity 100.0%; Pred. No. 5,4e-38; Mismatches 0; Indels 0; Gaps 0;

Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGAGTAAAGGACTTAACTTGTAACTAACTAAAGGGGAACCTCTAGTAGA 60
 1 GCCTGAGTAAAGGACTTAACTTGTAACTAACTAAAGGGGAACCTCTAGTAGA 60
 Db 1 GCCTGAGTAAAGGACTTAACTTGTAACTAACTAAAGGGGAACCTCTAGTAGA 60
 QY 61 CAATCCCGTGAATTAATATACAGATGCTTGAATGCGCTTGAGATTAATGCTTAAC 120
 61 CAATCCCGTGAATTAATATACAGATGCTTGAATGCGCTTGAGATTAATGCTTAAC 120
 Db 61 CAATCCCGTGAATTAATATACAGATGCTTGAATGCGCTTGAGATTAATGCTTAAC 120
 QY 121 GACTATCCCTT 131
 121 GACTATCCCTT 131
 Db 121 GACTATCCCTT 131

RESULT 4

ALA43033 ID ALA43033 standard; DNA; 131 BP.

ALA43033;

25-SEP-2002 (first entry)

Regulatable, catalytically active nucleic acid construction oligo #3.

Regulatable, catalytically active nucleic acid; RCANA; ribozyme;

gene therapy; ds.

Synthetic.

Key Location/Qualifiers

misc_feature 77 /*tag= a

108 /*note= "represents between 1 and 4 unknown nucleotides"

/*tag= b

/*note= "represents between 1 and 4 unknown nucleotides"

MO200196559-A2.

14-JUN-2001; 2001MO-US19302.

15-JUN-2000; 2000US-212097P.

(TEXA) UNIV TEXAS SYSTEM.

Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;

Davidson E, Cox JC, Reidel T;

WPI: 2002-122216/16.

New regulatable, catalytically active nucleic acids (RCANA), useful in

gene therapy (particularly for regulating gene expression), or in

assays for detecting the presence of ligands or activation of an

effector of RCANA

Example 2; Page 42; 126pp; English.

The present invention relates to regulatable, catalytically active

nucleic acids (RCANAs) which are regulated by polypeptides. These are

useful for regulating gene expression, in assays for detecting the

presence of ligands, for activation of an effector of RCANA, and in gene

therapy. The present sequence is an oligonucleotide used in the

construction of an RCANA.

Sequence 131 BP; 37 A; 32 C; 24 G; 36 T; 2 other;

Query Match 97.3%; Score 127.4; DB 24; Length 131;

Best Local Similarity 97.7%; Pred. No. 1.1e-36; Mismatches 3; Indels 0; Gaps 0;

Matches 128; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCTGAGTAAAGGACTTAACTTGTAACTAACTAAAGGGGAACCTCTAGTAGA 60
 1 GCCTGAGTAAAGGACTTAACTTGTAACTAACTAAAGGGGAACCTCTAGTAGA 60
 Db 1 GCCTGAGTAAAGGACTTAACTTGTAACTAACTAAAGGGGAACCTCTAGTAGA 60
 QY 61 CAATCCCGTGAATTAATATACAGATGCTTGAATGCGCTTGAGATTAATGCTTAAC 120
 61 CAATCCCGTGAATTAATATACAGATGCTTGAATGCGCTTGAGATTAATGCTTAAC 120
 Db 61 CAATCCCGTGAATTAATATACAGATGCTTGAATGCGCTTGAGATTAATGCTTAAC 120
 QY 121 GACTATCCCTT 131
 121 GACTATCCCTT 131
 Db 121 GACTATCCCTT 131

RESULT 5

ABN83048 ID ABN83048 standard; DNA; 131 BP.

ABN83048;

16-AUG-2002 (first entry)

Aptazyme construct oligonucleotide GpTtH6pool.

Aptazyme; regulatable; aptamer; luciferase; cyclic AMP; GpTtH6pool; ss.

Unidentified.

Key Location/Qualifiers

misc_feature 77 /*tag= a

108 /*note= "Base may be repeated 1-4 times"

/*tag= a

/*note= "Base may be repeated 1-4 times"

MO200196541-A2.

20-DEC-2001.

15-JUN-2001; 2001MO-US19119.

15-JUN-2000; 2000US-0661658.

(TEXA) UNIV TEXAS.

Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;

Davidson E, Cox JC, Reidel T;

WPI: 2002-090203/12.

Aptazyme construct for detecting the presence of ligands, comprises a

regulatable Group I intron aptamer oligonucleotide with a regulatory

domain, and modulates their kinetic parameters in response to an

effector

Claim 10; Page 31; 42pp; English.

The sequence represents an oligonucleotide used in the invention in the

construction of a group I regulatable aptazyme pool. The invention

relates to a novel aptazyme construct comprising a regulatable Group I

intron aptamer oligonucleotide sequence having an allosterically

regulatable regulatory domain, where the kinetic parameters of the

aptazyme on a target gene vary in response to the interaction of an

allosteric effector molecule with the regulatory domain, and the intron

splicing reaction occurs in vitro. The aptazyme is useful: (1) in assays

to detect the presence of ligands or to detect activation of an aptazyme

by an effector; (2) in the identification, isolation and enhancement of

allosteric effectors and of the allosterically regulatable aptazymes with

which they interact; (3) to activate or repress a reporter gene (e.g.

CC Luciferase) containing an engineered intron in response to an endogenous
CC activator; and (4) to monitor intracellular levels of proteins or small
CC molecules such as cyclic AMP.

XX Sequence 131 BP; 37 A; 32 C; 24 G; 36 T; 2 other;

Query Match 97.3%; Score 127.4; DB 24; Length 131;
Best Local Similarity 97.7%; Pred. No. 1.1e-36;
Matches 128; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCTGAGTATAAGTGACTTATCTGTAATCTATCTAAACGGGACCTCTAGTAGA 60
DB 1 GCCTGAGTATAAGTGACTTATCTGTAATCTATCTAAACGGGACCTCTAGTAGA 60
QY 61 CAATCCCGTGTAAATTAATATACAGCATGCTTGTATGCGCTTGGCAGATAATGCTTAC 120
DB 61 CAATCCCGTGTAAATTAATATACAGCATGCTTGTATGCGCTTGGCAGATAATGCTTAC 120
QY 121 GACTATCCCTT 131
DB 121 GACTATCCCTT 131

RESULT 6
AAL43050
ID AAL43050 standard; DNA; 133 BP.

AC AAL43050;

DT 25-SEP-2002 (first entry)

DE Regulatable, catalytically active nucleic acid construction oligo #9.

KM Regulatable catalytically active nucleic acid; RCANA; ribozyme;

OS Synthetic.

PN WO200196559-A2.

PD 20-DEC-2001.

PE 14-JUN-2001; 2001WO-US19302.

PR 15-JUN-2000; 2000US-212097P.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L,
PI Davidson E, Cox JC, Reidel T;

DR WPI; 2002-122216/16.

PS Example 5; Page 68; 126pp; English.
PT New regulatable, catalytically active nucleic acids (RCANA), useful in
PT gene therapy (particularly for regulating gene expression), or in
PT assays for detecting the presence of ligands or activation of an
PT effector of RCANA

CC The present invention relates to regulatable, catalytically active
CC nucleic acids (RCANAs) which are regulated by polypeptides. These are
CC useful for regulating gene expression, in assays for detecting the
CC presence of ligands, for activation of an effector of RCANA, and in gene
CC therapy. The present sequence is an oligonucleotide used in the
CC construction of an RCANA.

XX Sequence 133 BP; 37 A; 33 C; 25 G; 38 T; 0 other;

Query Match 83.2%; Score 109; DB 24; Length 133;
Best Local Similarity 98.5%; Pred. No. 5.8e-30;
Matches 131; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 GCCTGAGTATAAGTGACTTATCTGTAATCTATCTAAACGGGACCTCTAGTAGA 60
DB 1 GCCTGAGTATAAGTGACTTATCTGTAATCTATCTAAACGGGACCTCTAGTAGA 60
QY 61 CAATCCCGTGTAAATTAATATACAGCATGCTTGTATGCGCTTGGCAGATAATGCTTAC 118
DB 61 CAATCCCGTGTAAATTAATATACAGCATGCTTGTATGCGCTTGGCAGATAATGCTTAC 118
QY 119 AGCAGTATCCCTT 131
DB 121 AGCAGTATCCCTT 133

RESULT 7
AAL43052
ID AAL43052 standard; DNA; 129 BP.

AC AAL43052;

DT 25-SEP-2002 (first entry)

DE Regulatable, catalytically active nucleic acid construction oligo #11.

KM Regulatable catalytically active nucleic acid; RCANA; ribozyme;

OS Synthetic.

PN WO200196559-A2.

PD 20-DEC-2001.

PE 14-JUN-2001; 2001WO-US19302.

PR 15-JUN-2000; 2000US-212097P.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L,
PI Davidson E, Cox JC, Reidel T;

DR WPI; 2002-122216/16.

PS New regulatable, catalytically active nucleic acids (RCANA), useful in
PS gene therapy (particularly for regulating gene expression), or in
PS assays for detecting the presence of ligands or activation of an
PS effector of RCANA

XX Example 5; Page 68; 126pp; English.

CC The present invention relates to regulatable, catalytically active
CC nucleic acids (RCANAs) which are regulated by polypeptides. These are
CC useful for regulating gene expression, in assays for detecting the
CC presence of ligands, for activation of an effector of RCANA, and in gene
CC therapy. The present sequence is an oligonucleotide used in the
CC construction of an RCANA.

XX Sequence 129 BP; 36 A; 32 C; 24 G; 37 T; 0 other;

Query Match 81.7%; Score 107; DB 24; Length 129;
Best Local Similarity 98.5%; Pred. No. 3.1e-29;
Matches 129; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 GCCTGAGTATAAGTGACTTATCTGTAATCTATCTAAACGGGACCTCTAGTAGA 60
DB 1 GCCTGAGTATAAGTGACTTATCTGTAATCTATCTAAACGGGACCTCTAGTAGA 60
QY 61 CAATCCCGTGTAAATTAATATACAGCATGCTTGTATGCGCTTGGCAGATAATGCTTAC 120
DB 61 CAATCCCGTGTAAATTAATATACAGCATGCTTGTATGCGCTTGGCAGATAATGCTTAC 120
QY 121 GACTATCCCTT 131
DB 121 GACTATCCCTT 131

Db 119 GACTATCCCTT 129

RESULT 8
ID AAL43051 standard; DNA: 119 BP.

XX AAL43051:

XX 25-SEP-2002 (first entry)

XX Regulatable, catalytically active nucleic acid construction oligo #10.

XX Regulatable, catalytically active nucleic acid; RCANA; ribozyme;

XX gene therapy; ds.

XX Synthetic.

XX WO200196559-A2.

XX 20-DEC-2001.

XX 14-JUN-2001; 2001WO-US19302.

XX 15-JUN-2000; 2000US-212097P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;

XX Davidson E, Cox JC, Reidel T;

XX WPI; 2002-122216/16.

XX New regulatable, catalytically active nucleic acids (RCANA), useful in

XX gene therapy (particularly for regulating gene expression), or in

XX assays for detecting the presence of ligands or activation of an

XX effector of RCANA.

XX Example 5; Page 68; 126pp; English.

XX The present invention relates to regulatable, catalytically active

XX nucleic acids (RCANAs) which are regulated by polypeptides. These are

XX useful for regulating gene expression, in assays for detecting the

XX presence of ligands, for activation of an effector of RCANA, and in gene

XX therapy. The present sequence is an oligonucleotide used in the

XX construction of an RCANA.

XX Sequence 119 BP; 30 A; 32 C; 24 G; 33 T; 0 other;

XX Query Match 66.4%; Score 87; DB 24; Length 119;

XX Best Local Similarity 90.8%; Pred. NO. 6e-22;

XX Matches 119; Conservative 0; Mismatches 0; Indels 12; Gaps 2;

XX Db 109 GACTATCCCTT 119

RESULT 9
ID AAL43055 standard; DNA: 117 BP.

XX AAL43055:

XX 25-SEP-2002 (first entry)

XX Regulatable, catalytically active nucleic acid construction oligo #13.

XX Regulatable, catalytically active nucleic acid; RCANA; ribozyme;

XX gene therapy; ds.

XX Synthetic.

XX WO200196559-A2.

XX 20-DEC-2001.

XX 14-JUN-2001; 2001WO-US19302.

XX 15-JUN-2000; 2000US-212097P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;

XX Davidson E, Cox JC, Reidel T;

XX WPI; 2002-122216/16.

XX New regulatable, catalytically active nucleic acids (RCANA), useful in

XX gene therapy (particularly for regulating gene expression), or in

XX assays for detecting the presence of ligands or activation of an

XX effector of RCANA.

XX Example 5; Page 69; 126pp; English.

XX The present invention relates to regulatable, catalytically active

XX nucleic acids (RCANAs) which are regulated by polypeptides. These are

XX useful for regulating gene expression, in assays for detecting the

XX presence of ligands, for activation of an effector of RCANA, and in gene

XX therapy. The present sequence is an oligonucleotide used in the

XX construction of an RCANA.

XX Sequence 117 BP; 30 A; 31 C; 23 G; 33 T; 0 other;

XX Query Match 66.0%; Score 86.4; DB 24; Length 117;

XX Best Local Similarity 89.2%; Pred. NO. 9.8e-22;

XX Matches 107; Conservative 0; Mismatches 6; Indels 7; Gaps 1;

XX Db 61 CAATCCCGTGTCTTATACGAGCAGTCGCTTGAGCCCTTGCGAGTAAATGCTTAC 120

RESULT 10
ID AAL43054 standard; DNA: 115 BP.

XX AAL43054:

XX 25-SEP-2002 (first entry)

XX Regulatable, catalytically active nucleic acid construction oligo #12.

XX Regulatable, catalytically active nucleic acid; RCANA; ribozyme;

XX gene therapy; ds.

XX Synthetic.

XX WO200196559-A2.

XX 20-DEC-2001.

XX 14-JUN-2001; 2001WO-US19302.

```

PR      15-JUN-2000; 2000US-212097P.
XX
XX      (TEXA ) UNIV TEXAS SYSTEM.
XX
PI      Ellington AD, Hesselbergh J, Marshall K, Robertson M, Sooter L,
PI      Davidson E, Cox JC, Reidel T;
XX
XX      WPI; 2002-122216/16;
XX
PT      New regulatable, catalytically active nucleic acids (RCANA), useful in
PT      gene therapy (particularly for regulating gene expression), or in
PT      assays for detecting the presence of ligands or activation of an
PT      effector of RCANA -
XX
PS      Example 5; Page 68; 126pp; English.
XX
CC      The present invention relates to regulatable, catalytically active
CC      nucleic acids (RCANAs) which are regulated by polypeptides. These are
CC      useful for regulating gene expression in assays for detecting the
CC      presence of ligands, for activation of an effector of RCANA, and in gene
CC      therapy. The present sequence is an oligonucleotide used in the
CC      construction of an RCANA.
XX
SQ      Sequence 115 BP; 30 A; 30 C; 22 G; 33 T; 0 other;
Query Match          63.7%; Score 83.4; DB 24; Length 115;
Best Local Similarity 91.9%; Pred. No. 1.2e-20;
Matches 102; Conservative 0; Mismatches 1; Indels 8; Gaps 1;
QY      1 GCCTGATATAAGGTGACTTATCTATTCTATCTAAACGGGAACTCTCTAGTAGA 60
DB      1 GCCCGATATAAGGTGACTTATCTATTCTATCTAAACGGGAACTCTCTAGTAGA 60
QY      61 CAATCCCCTGCTAAATTATACAGCATCCTTGATGCCCTGGAGATAA 111
DB      61 CAATCCCG-----TATACCAGCATCGTCTTGATGCCCTTGGCAGCTAA 103
RESULT 11
ALAL3067
ID      ALAL3067 standard; RNA; 82 BP.
XX
XX      ALAL3067;
AC
DE      25-SEP-2002 (first entry)
XX
XX      Regulatable, catalytically active nucleic acid #2.
XX
XX      Regulatable catalytically active nucleic acid; RCANA; ribozyme;
XX      gene therapy; ss.
OS
OS      Unidentified.
XX
FH      Key
FT      misc_binding Location/Qualifiers
FT      /tag= a 4..8
FT      /bound_moiety= "binds nucleotides 33-29 of itself"
FT      stem_loop 14..24
FT      /tag= b 29..33
FT      /bound_moiety= "binds nucleotides 8-4 of itself"
FT      misc_binding 34..35
FT      /tag= d
FT      /bound_moiety= "binds nucleotides 79-78 of itself"
FT      misc_binding 41
FT      /tag= e
FT      /bound_moiety= "binds nucleotide 72 of itself"
FT      misc_binding 45..46
FT      /tag= f
FT      /bound_moiety= "binds nucleotides 68-67 of itself"
FT      stem_loop 48..62
FT      /tag= g

```

[illegible]

[illegible]

Accession	Location/Qualifiers
ABN83051;	
16-AUG-2002 (first entry)	
GpITH1P6.131 aptamer construct.	
Aptazyme; regulatable; aptamer; luciferase; cyclic AMP; ss;	
GpITH1P6.131.	
Unidentified.	
Key	
misc_binding	Location/Qualifiers
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	/*tag= a
	/bound_moiety= "Bases 33-28"
stem_loop	14..24
	/*tag= b
	28..33
	/*tag= c
	/bound_moiety= "Bases 9-4"
	34..35
	/*tag= c
	/bound_moiety= "Bases 79-78"
	41
	/*tag= d
	/bound_moiety= "Base 72"
	45..46
	/*tag= e
	/bound_moiety= "Bases 68-67"
	48..62
	/*tag= f
	67..68
	/*tag= g
	/bound_moiety= "Bases 46-45"
	72
	/*tag= h
	/bound_moiety= "Base 41"
	78..79
	/*tag= i
	/bound_moiety= "Bases 35-34"
Wo200196541-A2.	
20-DEC-2001.	
15-JUN-2001; 2001WO-US19119.	
15-JUN-2000; 2000US-0661658.	
(TEXA) UNIV TEXAS.	
Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;	
Davidson E, Cox JC, Reidel T;	
WPI; 2002-090203/12.	
Aptazyme construct for detecting the presence of ligands, comprises a	
regulatable Group I intron aptamer oligonucleotide with a regulatory	
domain, and modulates their kinetic parameters in response to an	
effector -	
Disclosure; Fig 2A; 42pp; English.	
The sequence represents the GpITH1P6.131 aptamer construct used in the	
Invention. The invention relates to a novel aptazyme construct comprising	
a regulatable Group I intron aptamer oligonucleotide sequence having an	
allosterically regulatable regulatory domain, where the kinetic	
parameters of the aptazyme on a target gene vary in response to the	
interaction of an allosteric effector molecule with the regulatory	
domain, and the intron splicing reaction occurs in vitro. The aptazyme is	
useful: (1) in assays to detect the presence of ligands or to detect	
activation of an aptazyme by an effector; (2) in the identification,	

CC Isolation and enhancement of allosteric effectors and of the
 CC allosterically regulatable aptazymes with which they interact; (3) to
 CC activate or repress a reporter gene (e.g. luciferase) containing an
 CC engineered intron in response to an endogenous activator; and (4) to
 CC monitor intracellular levels of proteins or small molecules such as
 CC cyclic AMP.

SO Sequence 82 BP; 24 A; 21 C; 16 G; 21 U; 0 other;

Query Match 62.6%; Score 82; DB 24; Length 82;
 Best Local Similarity 74.4%; Pred. No. 3.5e-20;
 Matches 61; Conservative 21; Mismatches 0; Indels 0; Gaps 0;

QY 37 TAAACGGGGAACCTCTCTAGTACATCCGCTAAATTAACGACATGCTCTGAT 96
 Db 1 UAAACGGGGAACCTCTCTAGTACATCCGCTAAATTAACGACATGCTCTGAT 96
 61 GCGCTTGGCAGATAAATGCGCTA 118
 61 GCGCTTGGCAGATAAATGCGCTA 82

RESULT 14

AL43058
 ID AAL43058 standard; DNA; 107 BP.

AC AAL43058;

DT 25-SEP-2002 (first entry)

DE Regulatable, catalytically active nucleic acid construction oligo #16.

KW Regulatable catalytically active nucleic acid; RCANA; ribozyme;

OS Synthetic.

PN WO200196559-A2.

PD 20-DEC-2001.

PF 14-JUN-2001; 2001WO-US19302.

PR 15-JUN-2000; 2000US-212097P.

PS (TEXA) UNIV TEXAS SYSTEM.

PI Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;
 Davidson E, Cox JC, Reidel T;

DR WPI: 2002-122216/16.

PT New regulatable, catalytically active nucleic acids (RCANA), useful in
 assays for detecting the presence of ligands or activation of an
 effector of RCANA

CC Example 5; Page 69; 126pp; English.

CC The present invention relates to regulatable, catalytically active
 CC nucleic acids (RCANAs) which are regulated by polypeptides. These are
 CC useful for regulating gene expression, in assays for detecting the
 CC presence of ligands, for activation of an effector of RCANA, and in gene
 CC therapy. The present sequence is an oligonucleotide used in the
 CC construction of an RCANA.

SO Sequence 107 BP; 31 A; 28 C; 19 G; 29 T; 0 other;

Query Match 62.1%; Score 81.4; DB 24; Length 107;
 Best Local Similarity 97.2%; Pred. No. 6.3e-20;
 Matches 104; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 27 GTAATCTTCTAAACGGGGAACCTCTCTAGTACATCCGCTAAATTAACGACG 85

Db 1 GTAAATCTTCTAAACGGGGAACCTCTCTAGTACATCCGCTAAATTAACGACG 60
 QY 86 ATGCTTGTGATGCCATGTGCGACGATAAATGCTAACTATTCCTT 131
 Db 61 ATGCTTGTGATGCCATGTGCGACGATAAATGCTAACTATTCCTT 107

RESULT 15

AL43044
 ID AAL43044 standard; DNA; 122 BP.

AC AAL43044;

DT 25-SEP-2002 (first entry)

DE Regulatable, catalytically active nucleic acid construction oligo #5.

KW Regulatable catalytically active nucleic acid; RCANA; ribozyme;

OS Synthetic.

PN WO200196559-A2.

PD 20-DEC-2001.

PF 14-JUN-2001; 2001WO-US19302.

PR 15-JUN-2000; 2000US-212097P.

PS (TEXA) UNIV TEXAS SYSTEM.

PI Ellington AD, Hesselberth J, Marshall K, Robertson M, Sooter L;
 Davidson E, Cox JC, Reidel T;

DR WPI: 2002-122216/16.

PT New regulatable, catalytically active nucleic acids (RCANA), useful in
 assays for detecting the presence of ligands or activation of an
 effector of RCANA

CC Example 5; Page 67; 126pp; English.

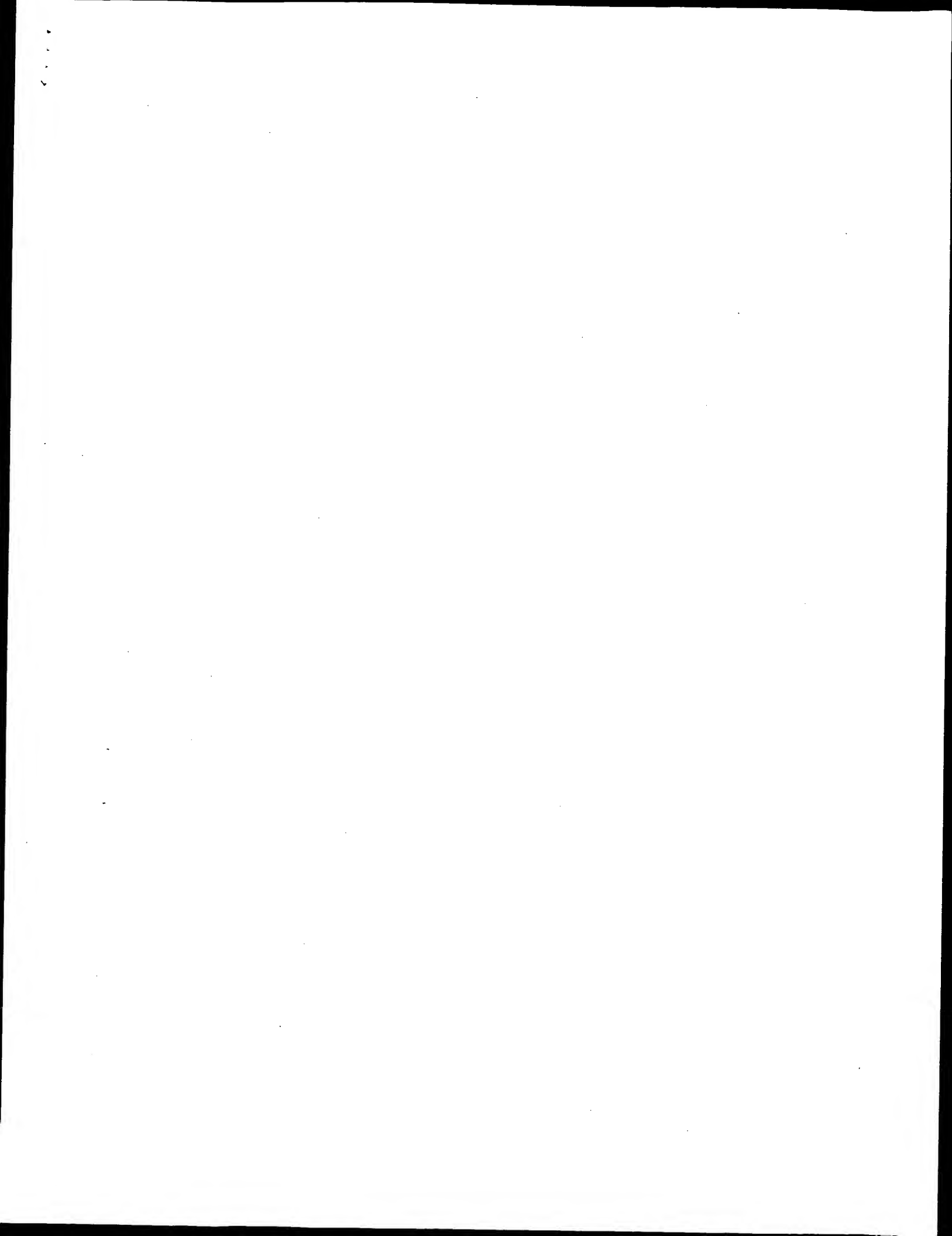
CC The present invention relates to regulatable, catalytically active
 CC nucleic acids (RCANAs) which are regulated by polypeptides. These are
 CC useful for regulating gene expression, in assays for detecting the
 CC presence of ligands, for activation of an effector of RCANA, and in gene
 CC therapy. The present sequence is an oligonucleotide used in the
 CC construction of an RCANA.

SO Sequence 122 BP; 34 A; 29 C; 24 G; 35 T; 0 other;

Query Match 61.5%; Score 80.6; DB 24; Length 122;
 Best Local Similarity 82.4%; Pred. No. 1.3e-19;
 Matches 108; Conservative 0; Mismatches 14; Indels 9; Gaps 1;

QY 1 GCGTGAATTAAGGAGCTATCTTGAATCTTAAACGGGGAACCTCTAGTAGA 60
 Db 1 GCGTGAATTAAGGAGCTATCTTGAATCTTAAACGGGGAACCTCTAGTAGA 60
 QY 61 CAATCCCGCTAAATTAATTAACGATGCTGATGCGCTTGGCAGATAAATGCGCTAAC 120
 Db 61 CAATCCCGCTAAATTAATTAACGATGCTGATGCGCTTGGCAGATAAATGCGCTAAC 120
 QY 121 GACTATCCCTT 131
 Db 112 GACTATCCCTT 122

Search completed: July 13, 2003, 22:15:21
 Job time: 149 secs



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 13, 2003, 21:34:47 ; Search time 1135 seconds
(without alignments)
1869.259 Million cell updates/sec

Title: US-09-661-658b-2

Perfect score: 131
Sequence: 1 gctctagatataagtgactt.....atgcttaagactatccctt 131

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: EST:*
2: em_estdb:*
3: em_esthm:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_hnv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	32.8	25.0	525	17 BH280107	BH280107 CH230-117
2	31.6	24.1	443	10 AW989880	AW989880 u19h10.y
3	31.6	24.1	1068	11 AK017255	AK017255 Mus muscu
4	31.2	23.8	682	17 BH245494	BH245494 PSB0764 S
5	31	23.7	570	17 AQ060314	AQ060314 CIT-HSP-2
6	30.8	23.5	340	17 AZ489123	AZ489123 1M0319E14

7	30.6	23.4	1004	17 CNS049YL	AL281190 Tetraodon
8	30	22.9	584	17 AZ742331	AZ742331 RPI-24-6
9	29.6	22.6	601	17 AQ461684	AQ461684 HS_5208-A
10	29.4	22.4	268	17 AQ239325	AQ239325 RPI11-68
11	29.4	22.4	492	14 L26622	L26622 MUSH033A.1a
12	29.4	22.4	565	17 AQ628517	AQ628517 CTBT-El-
13	29.2	22.3	371	14 D63293	D63293 HUM519C108
14	29	22.1	414	14 BQ634483	BQ634483 NKXV06_E
15	29	22.1	545	17 AZ159311	AZ159311 SP_0062-B
16	29	22.1	568	17 AT265148	AT265148 u103909.Y
17	28.8	22.0	451	17 BH732140	BH732140 BOMB64TF
18	28.8	22.0	1029	17 CNS05LKS	AL342878 Tetraodon
19	28.6	21.8	281	17 BH158201	BH158201 RPI18201
20	28.6	21.8	500	17 BH407444	BH407444 K607177-3
21	28.6	21.8	620	17 BH126169	BH126169 RPI-24-2
22	28.6	21.8	803	17 AQ030012	AQ030012 Pan tlog1
23	28.4	21.7	150	9 AA382203	AA382203 EST95373
24	28.4	21.7	491	17 A2031655	A2031655 RPI-23-2
25	28.4	21.7	560	17 AQ601442	AQ601442 HS_2096.A
26	28.4	21.7	563	17 BF647865	BF647865 BOCG377E
27	28.4	21.7	638	12 BF647865	BF647865 NF038A09E
28	28.4	21.7	674	17 BH531194	BH531194 BOCGWA0TR
29	28.4	21.7	882	12 BP120755	BP120755 601758145
30	28.4	21.7	868	17 CNS03609	AL243234 Tetraodon
31	28.4	21.7	1029	17 CNS01X05	AL172166 Tetraodon
32	28.2	21.5	386	10 AV936181	AV936181 AV936181
33	28.2	21.5	399	13 BJ276119	BJ276119 BJ276119
34	28.2	21.5	428	14 BQ788526	BQ788526 WT019.Whe
35	28.2	21.5	458	14 BQ243052	BQ243052 Taet150196
36	28.2	21.5	479	13 BG945339	BG945339 PMO-AN008
37	28.2	21.5	480	9 AL499891	AL499891 AL499891
38	28.2	21.5	619	14 BQ619850	BQ619850 Tair-1151A
39	28.2	21.5	639	10 BE566390	BE566390 601339986
40	28.2	21.5	672	13 BJ253216	BJ253216 BJ253216
41	28.2	21.5	709	6 BQ238482	BQ238482 TAE05003F
42	28.2	21.5	712	13 BJ311709	BJ311709 BJ311709
43	28.2	21.5	755	12 BF184543	BF184543 601842850
44	28.2	21.5	835	17 AZ544758	AZ544758 ENTF944TR
45	28	21.4	377	14 C66385	C66385 C66385 Yuj1

ALIGNMENTS

RESULT 1
LOCUS BH280107 525 bp DNA linear GSS 30-NOV-2001
DEFINITION CH230-117E23, TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
ACCESSION BH280107
VERSION BH280107.1 GI:17192509
KEYWORDS GSS.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 525)
Zhao,S., Shetty,D., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
,A., Gebregeorgis,E., Overton,U., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other GSS: CH230-117E23.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library

LOCUS	570 bp	DNA	linear	653 nt	653 nt
LOCUS	570 bp	DNA	linear	653 nt	653 nt
DEFINITION	CIT-HSP-235103.TR	CIT-HSP	Homo sapiens	genomic clone	235103, DNA
DEFINITION	sequence.				

ACCESSION A0060314
 VERSION A0060314.1 GI:3362567
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 570)
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
 Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
 Simon,M., and Venter,J.C.
 Use of a random BAC End Sequence Database for Sequence-Ready Map
 Building (1998)
 TITLE Unpublished (1998)
 JOURNAL COMMENT Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends.
 FEATURES
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 /organism="Homo sapiens"
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 /sex="Male"
 /cell_type="Sperm"
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 HindIII"
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 Best Local Similarity 62.0%; Pred. No. 7.1;
 Matches 49; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
 QY 10 TAAGTGACTTACTTGAATCTATCTAAACGGGACCTCTCTAGTACATCCCGT 69
 Db 375 TCATGTTATTTATGCTTAAATCTGTATGCGTGTATCATCTTATGATCTTGCATAT 434
 QY 70 GCTAATTATACAGCATC 88
 Db 435 GTTAACATATCCCTGCATC 453
 RESULT 6
 A2489123 340 bp DNA linear GSS 05-OCT-2000
 LOCUS 1M0319E14R Mouse 10kb plasmid UNGC1M library Mus musculus genomic
 ACCESSION A2489123
 VERSION A2489123
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 340)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
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 Seq primer: CACACAGAAACACACTATGACC
 Class: plasmid ends
 High quality sequence stop: 340.
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 /clone_id="UNGCM0319E14"
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 /sex="Male"
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 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 inducible derivative of plasmid R1. A copy-number
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."
 BASE COUNT 105 a 66 c 34 g 135 t
 ORIGIN
 Query Match 23.5%; Score 30.8; DB 17; Length 340;
 Best Local Similarity 58.9%; Pred. No. 6.5;
 Matches 53; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
 QY 21 ATACTGTATCTATCTAAACGGGACCTCTCTAGTACATCCCGTAAATTATA 80
 Db 165 ATATCTTATCTATCTAAATCTTACCATTTCCAGAGGCTGCTTTTCCATCATC 224
 QY 81 CCAGCATCGCTTGATGCGCTTGCGCATTA 110
 Db 225 CACTCTTGTGTTTACTCTCTTGGAGAA 254
 RESULT 7
 CNS049YL 1004 bp DNA linear GSS 21-MAY-2000
 LOCUS 094B11 of library G from Tetradon nigroviridis, genomic survey
 DEFINITION
 CNS049YL 1004 bp DNA linear GSS 21-MAY-2000
 ACCESSION AL281190.1 GI:8019499
 VERSION AL281190.1
 KEYWORDS GSS: genome survey sequence.
 SOURCE Tetradon nigroviridis.
 ORGANISM Tetradon nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Tetraodontidae; Tetraodon.
 REFERENCE 1 (bases 1 to 1004)
 AUTHORS Roost-Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,

For more information, please contact:
 Email: szhao@igr.org
 Clones are derived from the mouse BAC library RPI-24. For BAC clones availability, please contact Pieter de Jong (pdejong@email.cho.org). Clones may be purchased from BACPAC resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end

FEATURES	Location
source	1. . 601

Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCT-24. For BAC library availability, please contact Pieter de Jong (pdejong@small.chori.org). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/orderingframe.html>). BAC end

[illegible]

RESULT 10	
A0239325	
LOCUS	
DEFINITION	A0239325
LOCUS	268 bp DNA
DEFINITION	RpCt11-68A11.7K RpCt-11 Homo sapiens genomic clone RpCt-11-68A11, GSS 21-APR-1999
ACCESSION	A0239325
VERSION	A0239325.1
KEYWORDS	GSS.
KEYWORDS	GI:3671616
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE
AUTHORS
1. Lemaire, J. Euthelia: Primates, Catarrhini, Hominoidea, Homo.
1 (bases 1 to 268)
Barry, M.D., Granger, S.D., Zhao, S., Bass, S., Linher, K., Golden, R.,
use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
Comments: RPI11-68A11.TJ
Contact: Mark Adams
Department

The Institute for Eukaryotic Genomics
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: 77
Class: BAC ends.

FEATURES					
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			/clone_1lb="RPCI-11"		
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			/cell_type="Lymphocytes"		
BASE COUNT			/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;		
ORIGIN	92 a		RPC11 Human Male BAC Library"		
	37 c	41 g		97 t	1 other

	Indels	Gaps
Oy	4/7	0
Db	24	60
Oy	61	83
Db	84	104
	127	

RESULT 11	
L26622/c	
LOCUS	
DEFINITION	126622
	MUSBO33A lambda unizap male testis mRNA sequence.
ACCESSION	126622
VERSION	126622.1 GI:437412
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	

REFERENCE
1 (bases 1 to 492)
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
FEATURES
source

Maniatis; Euthalia; Rodentia; Schizothamnus; Vertebrata; Euteleostomi; Murinae; Muridae; Murinae; Mus
Kerr, S.M., Vamprle, S., McKay, S.J. and Cooke, H.J.
Analysis of cDNA sequences from mouse testis
Mamm. Genome 5, 557-565 (1994)
95093181
Contact: Kerr, S.M., Vamprle, S., McKay, S.J. and Cooke, H.J.
Location/Qualifiers
1..492

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Query Match
Best Local Similarity 22.4%; Score 29.4; DB 14; Length 492;
Matches 48; Conservative 0; W:1.00;
BASE COUNT 181 a 87 c 69 g 150 t 5 others
ORIGIN

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		nt	inlets	0:	Gaps	0:
Oy	34	ATCTAAAGGGGAACCTCTTAGTACACAATCCCGCTCAATTATTAACGACGTCTTT	93			
Dd	79	ATCTGATATGGAAAAAATCACCAGTAGCATTCACACTAGAAATGTTCTTGCTGTAA	20			
Oy	94	GATGCCCTGGGAGATAAA	112			
Dd	19	ATTTCCTTGCACGATACA	1			

RESULT 12	
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LOCUS	
DEFINITION	AO628517
VERSION	CITR1-El-2653G12.TF CITR1-El
KEYWORDS	DNA sequence.
SOURCE	AO628517.1 GI:5090909
ORGANISM	GSS.
	human.
	Homo sapiens
	565 bp DNA linear GSS:16-UN-1999
	genomic clone 2653G12,

REFERENCE AUTHORS	TITLE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (pass 1 to 565)	
Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and Venter, J.C.	Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building

Query Match	22.3%	Score 29.2;	DB 14;	Length 3.1;
Best Local Similarity	62.2%	Pred. No. 24;		
% of Sequences	0.1	Mismatches	28;	Indels 0;
				Gaps 0;

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	Best Local Similarity	62.2%;	Pred. No. 24;		
Matches	46;	Conservative	0;	Mismatches	28;
				Indels	0;
				Gaps	0;
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Ddb	191 AATATTTCATTTATCCCATGACTTAATAAATTACTGCATTATCTTAATACAAAGGC	132			
QY	106 AGATTAATGCCCTAA	119			
Ddb	131 AAGTAATGACCAA	118			

RESULT 14

[illegible]

Sederoff, R.
 Molecular Basis of Wood Formation in the Pine Megagenome
 Unpublished (2000)

COMMENT	Contact: Johnson, Arthur North Carolina State University Tel: 919 515 7800 Fax: 919 515 7801 Email: a.johnson@unity.ncsu.edu Seq primer: T3. Location/Qualifiers 1. .414
FEATURES	
source	

FEATURES
SOURCE

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/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina
/db_xref="taxon:3352"
/clone="NXRV069_E06"
/clone_lib="NXRV (NsF Xylem Root wood Vertical)"
/tissue_type="Xylem"
/cell_type="Root (Primary)"
/dev_stage="Transitional"
/lab_host="XLI-Blue"
/note="Vector: pBluescript SK-; Site_1: Eco RI; Site_2:
XhoI. The library is from primary xylem scraped from the
roots of a twelve year old tree in the transitional phase
from juvenile wood to mature wood production. NOTE: The
sequences contain a 'CDNA adaptor' between the EcoRI site
and the start of the EST. The adaptersequence is
'AATCGGCACGAG'. "
```

Quer
Best
Matc

QY 4 TGAGTATAAGGTGACTTATACCTGTGATCTATCTAATCTAAACGGGGAACCTCTCTGTATGACCA 63
 ||||| - - - - - ||||| - - - - - ||||| - - - - - ||||| -
 Db 64 TGACCAGAGATGGAAATATATGATCTAATGATGACAGAGAAACACCAACTAGACTTA 120
 - - - - - ||||| - - - - - ||||| - - - - - ||||| - - - - - ||||| -

FEATURES	Location/qualifiers
source	1. .371

Db 124 TTACCAACAAATATTTTATAAAGCCCTGATTTAAATTTGTTGATAAA 1/4

BASE CO
ORIGIN

LOCUS	A2159311	545 bp	DNA	Linear	GSS 29-AUG-2000

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using SW model
 July 13, 2003, 19:59:57 (Search time 37 seconds
 (without alignments) updates/sec
 1085.802 Million cell

ME-09-661-658B-2

Sequence: IDENTITY_NUC Canext 1.0

Scoring table: Gapop 10.0 , 153338381 residues

Searched: 1 hits satisfying chosen par-

Total number of elements: 0

Maximum DB	Match
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100%	100%

Maximum first 45 Summer
listing

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3: /cgn2.6/ptodata1/1/ina/6B.COMB.seq.*
4: /cgn2.6/ptodata1/1/ina/PCTUS.COMB.seq.*

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number of results predicted by chance to have a
the score of the result being printed
distribution.

Description

No.	Score	Match	Length	US-08-251-8968B-1	Sequence 24, Appl
1	78.4	58.8	510	US-09-257-503A-30	Sequence 27, Appl
2	37.2	28.4	59	US-09-257-503A-29	Sequence 28, Appl
3	37.2	28.4	123	US-09-257-503A-28	Sequence 29, Appl
4	37.2	28.4	125	US-09-257-503A-28	Sequence 36, Appl
5	37.2	28.4	149	US-08-443-957-29	Sequence 37, Appl
6	31.4	24.3	42	US-08-443-957-37	Sequence 20, Appl
7	30.4	22.2	38	US-08-443-957-6	Sequence 1, Appl
8	30.4	22.2	40	US-08-823-852-20	Sequence 1, Appl
9	28.4	21.7	5140	US-09-052-888-88	Sequence 1, Appl
10	28.4	21.7	5140	US-08-887-352B-1	Sequence 89, Appl
11	28.4	21.7	6127	US-09-206-005-1	Sequence 5, Appl
12	28.4	21.7	6127	US-08-468-819-89	Sequence 33, Appl
13	28.4	20.9	6127	US-08-468-819-89	Sequence 9, Appl
14	27.4	20.9	1185	US-09-4293-638-5	Sequence 4, Appl
15	27.4	20.9	59	US-09-251-503A-33	Sequence 7, Appl
16	25.2	19.8	1558	US-07-891-942G-9	Sequence 12, Appl
17	25.2	19.2	1886	US-07-891-942G-4	Sequence 1, Appl
18	25.2	19.2	1920	US-09-356-952-12	Sequence 19, Appl
19	25.2	19.2	43676	US-09-026-075-1	Sequence 11, Appl
20	24.8	18.9	6243	US-09-221-117B-11	Sequence 11, Appl
21	24.6	18.8	660	US-08-566-459A-11	Sequence 11, Appl
22	24.6	18.8	8220	US-08-487-826B-11	Sequence 11, Appl
23	24.6	18.8	8220	US-08-487-826B-13	Sequence 11, Appl
24	24.6	18.8	19124	US-08-487-826B-13	Sequence 11, Appl
25	24.6	18.8	1789	US-08-455-543A-29	Sequence 29, Appl
26	24.4	18.6	1		
27	24.4	18.6	1		

ALIGNMENTS

RESULT 1
US-08-431-896B-1
Application US/08431896B-1

Sequence 5773244
patent NO. INFORMATION:

GENERAL: Ares, Ethan E.
APPLICANT: Ford, RNA Cyclase Ribozymes

APPLICATION: 7
TITLE OF INVENTION:
OF SEQUENCES:

NUMBER: Address and Townsend and Townsend
CORRESPONDENCE: Townsend and Townsend
ADDRESS: Townsend Center, Eighteen
TOWNSEND: Townsend Center, Eighteen

ADDRESS: TWO EMBURY STREET: San Francisco

CITY: CALHOUN
STATE: USA
COUNTRY: USA

CO: 94111-3855
ZIP: 94111-3855
NUMBER READABLE FOR

COMPUTER TYPE: IBM PC
MEDIUM TYPE: IBM PC
MEDIUM: IBM PC

OPERATING SYSTEM: patentli
SOFTWARE: ION

CURRENT APPLICATION NUMBER 03-4

FILED DATE: 11/1/78
FILING OFFICE: NEW YORK
CLASSIFICATION: CONFIDENTIAL

PRIOR APPLICATION NUMBER
19-

FILING DATE	INFC
ATTORNEY/AGENT	KR

NAME: WEDER, J.
REGISTRATION NUM
SECRET

REFERENCE/COMMUNICATION

TELEPHONE: (415)
TELEFAX: (415)

INFORMATION CHARACTER
SEQUENCE

LENGTH: nucleic
TYPE: nucleic

STRANDED: 1 in
TOPOLOGY:
TYPE:

MOLECULE 1
; 08-431-896B-1

Query Match

Best Local 55; Cor
Matches

1 GCGTGG

—

1

Tue Jul 15 10:33:02 2003

us-09-661-658b-2.rni

Page 2

DB 341 GCCUGAGUADAAGUGACUUAACUCUUAUACUUAACGAGGAGCCUCUCUAGUAGA 400
OY 61 CAATCCGCTGCTTAATATATA 80
DB 401 CAATCCGCTGCTTAATATATA 80
RESULT 2
US-09-257-503A-30
Sequence 30, Application US/09257503A
Patent No. 6387617
GENERAL INFORMATION:
APPLICANT: ASHER, Nathan
TITLE OF INVENTION: CATALYTIC NUCLEIC ACID AND ITS MEDICAL USE
CURRENT APPLICATION NUMBER: US/09/257,503A
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: PCT/IL97/00282
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: IL119135
NUMBER OF SEQ ID NOS: 39
SOFTWARE: SEQ ID NOS: 39
SEQ ID NO 30 Patentln Ver. 2.1
LENGTH: 59
TYPE: RNA
ORGANISM: Humanus
US-09-257-503A-30

Query Match
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Matches 33; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

OY 29 AATCTATCTAAACGGGGAACCTCTCTAGTACACATCCCGTCTTAATATA 78
DB 4 AATCTATCTAAACGGGGAACCTCTCTAGTACACATCCCGTCTTAATATA 78
RESULT 3
US-09-257-503A-24
Sequence 24, Application US/09257503A
Patent No. 6387617
GENERAL INFORMATION:
APPLICANT: ASHER, Nathan
TITLE OF INVENTION: CATALYTIC NUCLEIC ACID AND ITS MEDICAL USE
CURRENT APPLICATION NUMBER: US/09/257,503A
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: PCT/IL97/00282
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: IL119135
NUMBER OF SEQ ID NOS: 39
SOFTWARE: SEQ ID NOS: 39
SEQ ID NO 24 Patentln Ver. 2.1
LENGTH: 123
TYPE: RNA
ORGANISM: Humanus
US-09-257-503A-24

Query Match
Best Local Similarity 28.4%; Score 37.2; DB 4; Length 123;
Matches 33; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

OY 29 AATCTATCTAAACGGGGAACCTCTCTAGTACACATCCCGTCTTAATATA 78
DB 4 AATCTATCTAAACGGGGAACCTCTCTAGTACACATCCCGTCTTAATATA 78

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Matches 33; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

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RESULT 5
US-09-257-503A-28
Sequence 28, Application US/09257503A
Patent No. 6387617
GENERAL INFORMATION:
APPLICANT: ASHER, Nathan
TITLE OF INVENTION: CATALYTIC NUCLEIC ACID AND ITS MEDICAL USE
CURRENT APPLICATION NUMBER: US/09/257,503A
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: PCT/IL97/00282
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: IL119135
NUMBER OF SEQ ID NOS: 39
SOFTWARE: SEQ ID NOS: 39
SEQ ID NO 28 Patentln Ver. 2.1
LENGTH: 149
TYPE: RNA
ORGANISM: Humanus
US-09-257-503A-28

Query Match
Best Local Similarity 28.4%; Score 37.2; DB 4; Length 149;
Matches 33; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

OY 29 AATCTATCTAAACGGGGAACCTCTCTAGTACACATCCCGTCTTAATATA 78
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OY 29 AATCTATCTAAACGGGGAACCTCTCTAGTACACATCCCGTCTTAATATA 78
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Query Match	23.2%	Score 30.4;	DB 1;	Length 40;
Best Local Similarity	68.8%	Pred. No. 0.013;		
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RESULT 9
US-08-825-852-20/c
; Sequence 20, Application US/08825852
; Patent No. 6121416
;
GENERAL INFORMATION:
APPLICANT: Clark, Ross G1
APPLICANT: Lowman, Henry B.
APPLICANT: Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
;
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,852
FILING DATE: 04-Apr-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 5140 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single

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Query Match	21.7%;	Score 28.4;	DB 3;	Length 5140;
Best Local Similarity	53.6%;	Pred. No. 0.55;		
Matches	59;	Conservative	0;	Mismatches 51.

QY	8	TATTAAGGACTTATACCTTGTAACTATCTAAACGGGAGCCCTCTATACACATGCC	67
Db	2436	TTTAAACAAAATTAAACCGAATTTTAAACAAATATTAACGTTTNCATTTCCGATCCT	2377
QY	68	GTGCTAAATTTACACAGCATGCTCTATCATCCCTGGACGAAATAACGCT	117
Db	2376	GGGGTAAAGCTCATCAGCTGCTGTGTTAAACGATTCACAGATATCTCTGCT	2322

US-09-052-888-20/c
Sequence 20, Application US/09052888
Patent No. 6251865

```

1  GENERAL INFORMATION:
2  APPLICANT: Clark, Ross GJ
3  APPLICANT: Lowman, Henry B.
4  APPLICANT: Robinson, Iain C.A.F.
5  TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
6  NUMBER OF SEQUENCES: 109
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE: Genentech, Inc.
9  STREET: 1 DNA Way
10 CITY: South San Francisco
11 STATE: California
12 COUNTRY: USA
13 ZIP: 94080
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
17
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: WinPatIn (Genentech)
21 CURRENT APPLICATION NUMBER: US/09/052,888
22 APPLICATION NUMBER: US/09/052,888
23 FILING DATE: 31-Mar-1998
24 CLASSIFICATION: 514
25
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Hasak, Janet E.
28 REGISTRATION NUMBER: 28,616
29 REFERENCE/DOCKET NUMBER: PI071P1
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: 650/225-1896
32 TELEFAX: 650/952-9881
33 INFORMATION FOR SEQ ID NO: 20:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 5140 base pairs
36 TYPE: Nucleic Acid
37 STRANDEDNESS: Single
38 TOPOLOGY: Linear
39
40 US-09-052-888-20

```

Query Match	21.7%;	Score	28.4;	DB	4;	Length	5140;
Best Local Similarity	53.6%;	Pred. No.	0	55.			

	Indels	Gaps
QY 8 TATAAGTCACCTATACCTGTATCTATCTAAACGGGAAACCTCTGTAGTACACATCCCC	67	
Db 2436 TTTAACAAAATTTTACGCGCAATTTTAAACAAAATATTAAGCTTTACAAATTTCCGATCCT	2377	
QY 68 GTGCTAATTTATACGACATGCTGTATGCCCTTGGCAGATAAAGCCT	117	
Db 2376 GGGGTAAGCTCATCAGCGTGTGCTGAACGATTTACAGATGTCTGCT	2327	

RESULT 11
US-08-887-352B-1/c
; Sequence 1, Application US/08887352B

Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Syvoda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6127 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Circular
US-08-887-352B-1

Query Match 21.7%; Score 28.4; DB 2; Length 6127;
Best Local Similarity 53.6%; Pred. No. 0.59;
Matches 59; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 8 TATAAGTGACTTATACCTGTGATCTATCTAATACGGGAGACCTCTCTAGTACAAATCCC 67
DB 3423 TTTAACAAAATTTTAAACGGGAAATTTTAAACAAATTTTAAACGTTTCCGATCCT 3364
QY 68 GTGCTAATTTATACGACATCGTCTTGATGCCCTTGCGAGATAATGCT 117
DB 3363 GCGGTAAAGCTATCAGCGTGTCTGTGAAGCATTCACAGATGTCTGCT 3314

RESULT 12
US-09-109-207C-1/C
Sequence 1, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 1
LENGTH: 6127
TYPE: DNA
ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial
LOCATION: 1-6127
OTHER INFORMATION: Expression plasmid
US-09-109-207C-1

Query Match 21.7%; Score 28.4; DB 4; Length 6127;
Best Local Similarity 53.6%; Pred. No. 0.59;
Matches 59; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
QY 8 TATAAGTGACTTATACCTGTGATCTATCTAATACGGGAGACCTCTCTAGTACAAATCCC 67
DB 3423 TTTAACAAAATTTTAAACGGGAAATTTTAAACAAATTTTAAACGTTTCCGATCCT 3364
QY 68 GTGCTAATTTATACGACATCGTCTTGATGCCCTTGCGAGATAATGCT 117
DB 3363 GCGGTAAAGCTATCAGCGTGTCTGTGAAGCATTCACAGATGTCTGCT 3314
RESULT 13
US-09-296-005-1/C
Sequence 1, Application US/09296005
Patent No. 6290957
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123C1r
CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 1
LENGTH: 6127
TYPE: DNA
ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial Sequence
LOCATION: 1-6127
OTHER INFORMATION: Expression plasmid
US-09-296-005-1

Query Match 21.7%; Score 28.4; DB 4; Length 6127;
Best Local Similarity 53.6%; Pred. No. 0.59;
Matches 59; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 8 TATAAGTGACTTATACCTGTGATCTATCTAATACGGGAGACCTCTCTAGTACAAATCCC 67
DB 3423 TTTAACAAAATTTTAAACGGGAAATTTTAAACAAATTTTAAACGTTTCCGATCCT 3364
QY 68 GTGCTAATTTATACGACATCGTCTTGATGCCCTTGCGAGATAATGCT 117
DB 3363 GCGGTAAAGCTATCAGCGTGTCTGTGAAGCATTCACAGATGTCTGCT 3314

RESULT 14
US-08-468-819-89/C
Sequence 89, Application US/08468819
Patent No. 5871723
GENERAL INFORMATION:
APPLICANT: Strieter, Robert M.
APPLICANT: Polyneri, Peter J.
APPLICANT: Kunkel, Steven L.
TITLE OF INVENTION: CXG Chemokines as Regulators of
TITLE OF INVENTION: Angiogenesis
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

Query Match	20.9%	Score 27.4	DB 2	Length 297
Best Local Similarity	69.8%	Pred. No. 0.41		
Matches	37	Conservative	0	Mismatches 16; Indels 0; Gaps 0;
QY	52	TCTAGTACACATCCCGTCTAAATATTACACAGCATCGCTTGAGCCCTTG	104	
Db	288	TCTTTAGACATTCCTCTGCTACACGCTTACAGTAATCTTGATGCGCCTTG	236	

```

: LOCATION: 80..374
US-08-493-638-5

Query Match 20.9%, Score 27.4; DB 1; Length 1195;
Best Local Similarity 69.8%; Pred. No. 0.72;
Matches 37; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 52 TCTAGTAGACAAATCCCGTGTAAATTTATACAGCATGCTTTGATGCCCTTGG 104
   ||| ||||| ||| ||||| ||| ||| ||||| ||||| |||
Db 367 TCTTTTAGACATTTCTCTTGGTAACTGCTTTGAGTAATTCCTGATGGCCTTCG 315

```

RESULT 2
US-09-883-119A-20
; Sequence 20, Application US/09883119A

```

; Publication No. US20030104520A1
; GENERAL INFORMATION:
; APPLICANT: The University of Texas System Board of Regents
; TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
; FILE REFERENCE: 119927-1050
; CURRENT APPLICATION NUMBER: US/09/883,119A
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 60/212,097
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 131
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-883-119A-20

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Query Match
Best Local Similarity 100.0%; Score 131; DB 9; Length 131;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCCTGAGTATAAGTACTTATCTGTAATCTATCTAAACGGGAACTCTCTAGTAGA 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 1 GCCTGAGTATAAGTACTTATCTGTAATCTATCTAAACGGGAACTCTCTAGTAGA 60
QY 61 CAATCCCGTCTAAATTAATTAACAGCATGCTTGATGCCCTTGAGATAAATGCCCTAAC 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 61 CAATCCCGTCTAAATTAATTAACAGCATGCTTGATGCCCTTGAGATAAATGCCCTAAC 120
QY 121 GACTATCCCTT 131
   |||||||||||
DB 121 GACTATCCCTT 131

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RESULT 3

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US-09-883-119A-5
; Sequence 5, Application US/09883119A
; Publication No. US20030104520A1
; GENERAL INFORMATION:
; APPLICANT: The University of Texas System Board of Regents
; TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
; FILE REFERENCE: 119927-1050
; CURRENT APPLICATION NUMBER: US/09/883,119A
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 60/212,097
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 131
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Engineered Aptazyme
; NAME/KEY: misc.feature
; LOCATION: (77)-(177)
; OTHER INFORMATION: n-a,c,t, or g
; NAME/KEY: misc.feature
; LOCATION: (108)-(108)
; OTHER INFORMATION: n-a,c,t, or g
US-09-883-119A-5

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Query Match
Best Local Similarity 97.3%; Score 127.4; DB 9; Length 131;
Matches 128; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 GCCTGAGTATAAGTACTTATCTGTAATCTATCTAAACGGGAACTCTCTAGTAGA 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 1 GCCTGAGTATAAGTACTTATCTGTAATCTATCTAAACGGGAACTCTCTAGTAGA 60

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QY 61 CAATCCCGTCTAAATTAATTAACAGCATGCTTGATGCCCTTGAGATAAATGCCCTAAC 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 61 CAATCCCGTCTAAATTAATTAACAGCATGCTTGATGCCCTTGAGATAAATGCCCTAAC 120
QY 121 GACTATCCCTT 131
   |||||||||||
DB 121 GACTATCCCTT 131

```

RESULT 4

```

US-09-883-119A-21
; Sequence 21, Application US/09883119A
; Publication No. US20030104520A1
; GENERAL INFORMATION:
; APPLICANT: The University of Texas System Board of Regents
; TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
; FILE REFERENCE: 119927-1050
; CURRENT APPLICATION NUMBER: US/09/883,119A
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 60/212,097
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 133
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-883-119A-21

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```

Query Match
Best Local Similarity 83.2%; Score 109; DB 9; Length 133;
Matches 131; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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QY 1 GCCTGAGTATAAGTACTTATCTGTAATCTATCTAAACGGGAACTCTCTAGTAGA 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 1 GCCTGAGTATAAGTACTTATCTGTAATCTATCTAAACGGGAACTCTCTAGTAGA 60
QY 61 CAATCCCGTCTAAATTAATTAACAGCATGCTTGATGCCCTTGAGATAAATGCCCTAAC 118
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 61 CAATCCCGTCTAAATTAATTAACAGCATGCTTGATGCCCTTGAGATAAATGCCCTAAC 120
QY 119 AGGACTATCCCTT 131
   |||||||||||
DB 121 AGGACTATCCCTT 133

```

RESULT 5

```

US-09-883-119A-23
; Sequence 23, Application US/09883119A
; Publication No. US20030104520A1
; GENERAL INFORMATION:
; APPLICANT: The University of Texas System Board of Regents
; TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
; FILE REFERENCE: 119927-1050
; CURRENT APPLICATION NUMBER: US/09/883,119A
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 60/212,097
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 129
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-883-119A-23

```

```

Query Match
Best Local Similarity 81.7%; Score 107; DB 9; Length 129;
Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```


Matches 129: Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 GCCTGAGTATAGTGAAGTCTTACTTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60
 1 GCCTGAGTATAGTGAAGTCTTACTTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60
 Db 61 CAATCCCGTGTCTAAATTTATACAGCATGCTTGTATGCCCTTGGCAGATAATGCTTAC 120
 61 CAATCCCGTGTCTAAATTTATACAGCATGCTTGTATGCCCTTGGCAGATAATGCTTAC 118
 QY 121 GACTATCCCTT 131
 119 GACTATCCCTT 129
 Db

RESULT 6
 US-09-883-119A-22
 ; Sequence 22, Application US/09883119A
 ; Publication No. US20030104520A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The University of Texas System Board of Regents
 ; TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
 ; FILE REFERENCE: 119927-1050
 ; CURRENT APPLICATION NUMBER: US/09/883,119A
 ; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: 60/212,097
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 22
 ; LENGTH: 119
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide
 US-09-883-119A-22

Query Match 66.4%; Score 87; DB 9; Length 119;
 Best Local Similarity 90.8%; Pred. No. 1.3e-21;
 Matches 119: Conservative 0; Mismatches 0; Indels 12; Gaps 2;

QY 1 GCCTGAGTATAGTGAAGTCTTACTTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60
 1 GCCTGAGTATAGTGAAGTCTTACTTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60
 Db 61 CAATCCCGTGTCTAAATTTATACAGCATGCTTGTATGCCCTTGGCAGATAATGCTTAC 120
 61 CAATCCCGTGTCTAAATTTATACAGCATGCTTGTATGCCCTTGGCAGATAATGCTTAC 108
 QY 121 GACTATCCCTT 131
 109 GACTATCCCTT 119
 Db

RESULT 7
 US-09-883-119A-25
 ; Sequence 25, Application US/09883119A
 ; Publication No. US20030104520A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The University of Texas System Board of Regents
 ; TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
 ; FILE REFERENCE: 119927-1050
 ; CURRENT APPLICATION NUMBER: US/09/883,119A
 ; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: 60/212,097
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 25
 ; LENGTH: 117
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

OTHER INFORMATION: Oligonucleotide
 US-09-883-119A-25

Query Match 66.0%; Score 86.4; DB 9; Length 117;
 Best Local Similarity 89.2%; Pred. No. 2e-21;
 Matches 107: Conservative 0; Mismatches 6; Indels 7; Gaps 1;

QY 1 GCCTGAGTATAGTGAAGTCTTACTTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60
 1 GCCTGAGTATAGTGAAGTCTTACTTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60
 Db 61 CAATCCCGTGTCTAAATTTATACAGCATGCTTGTATGCCCTTGGCAGATAATGCTTAC 120
 61 CAATCCCGTGTCTAAATTTATACAGCATGCTTGTATGCCCTTGGCAGATAATGCTTAC 113
 QY 121 GACTATCCCTT 131
 119 GACTATCCCTT 129
 Db

RESULT 8
 US-09-883-119A-24
 ; Sequence 24, Application US/09883119A
 ; Publication No. US20030104520A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The University of Texas System Board of Regents
 ; TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
 ; FILE REFERENCE: 119927-1050
 ; CURRENT APPLICATION NUMBER: US/09/883,119A
 ; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: 60/212,097
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 24
 ; LENGTH: 115
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide
 US-09-883-119A-24

Query Match 63.7%; Score 83.4; DB 9; Length 115;
 Best Local Similarity 91.9%; Pred. No. 2.5e-20;
 Matches 102: Conservative 0; Mismatches 1; Indels 8; Gaps 1;

QY 1 GCCTGAGTATAGTGAAGTCTTACTTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60
 1 GCCTGAGTATAGTGAAGTCTTACTTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60
 Db 61 CAATCCCGTGTCTAAATTTATACAGCATGCTTGTATGCCCTTGGCAGATAATGCTTAC 111
 61 CAATCCCGTGTCTAAATTTATACAGCATGCTTGTATGCCCTTGGCAGATAATGCTTAC 103
 QY 121 GACTATCCCTT 131
 109 GACTATCCCTT 119
 Db

RESULT 9
 US-09-883-119A-30
 ; Sequence 30, Application US/09883119A
 ; Publication No. US20030104520A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The University of Texas System Board of Regents
 ; TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
 ; FILE REFERENCE: 119927-1050
 ; CURRENT APPLICATION NUMBER: US/09/883,119A
 ; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: 60/212,097
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 30
 ; LENGTH: 122
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide
 US-09-883-119A-30

Query Match 62.7%; Score 82.2; DB 9; Length 122;
Best Local Similarity 83.2%; Pred. No. 6,8e-20;
Matches 109; Conservative 0; Mismatches 13; Indels 9; Gaps 1;

OY 1 GCCTGAGTATAGGAGCTTATCTTGTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60
DB 1 GCCTGAGTATAGGAGCTTATCTTGTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60
OY 61 CAATCCCGTCTAAATATATACCAATCGCTTGATCCCTTGCGAGATTAATGCTTAAC 120
DB 61 CAATCCCGTCTAAATATATACCAATCGCTTGATCCCTTGCGAGATTAATGCTTAAC 111
OY 121 GACTATCCCTT 131
DB 112 GACTATCCCTT 122

RESULT 10

US-09-883-119A-28
Sequence 28, Application US/09883119A
Publication No. US20030104520A1
GENERAL INFORMATION:
APPLICANT: The University of Texas System Board of Regents
TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
FILE REFERENCE: 119927-1050
CURRENT APPLICATION NUMBER: US/09/883,119A
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: 60/212,097
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 28
LENGTH: 107
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: oligonucleotide
US-09-883-119A-28

Query Match 62.1%; Score 81.4; DB 9; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.3e-19;
Matches 104; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

OY 27 GTAATCTATCTAAACGGGGAACCTCTCTAGTAGACAATCCCGTCTAAATT-ATACCAGC 85
DB 1 GTAATCTATCTAAACGGGGAACCTCTCTAGTAGACAATCCCGTCTAAATTGATACCAGC 60
OY 86 ATCGTCTGATGCCCTTGCGAG-ATAAATGCCCTAAGCACTATCCCTT 131
DB 61 ATCGTCTGATGCCCTTGCGAGCAATGAATGCCCTAAGCACTATCCCTT 107

RESULT 11

US-09-883-119A-16
Sequence 16, Application US/09883119A
Publication No. US20030104520A1
GENERAL INFORMATION:
APPLICANT: The University of Texas System Board of Regents
TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
FILE REFERENCE: 119927-1050
CURRENT APPLICATION NUMBER: US/09/883,119A
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: 60/212,097
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 122
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Parental p6 construct
US-09-883-119A-16

Query Match 61.5%; Score 80.6; DB 9; Length 122;
Best Local Similarity 82.4%; Pred. No. 2.6e-19;
Matches 108; Conservative 0; Mismatches 14; Indels 9; Gaps 1;

OY 1 GCCTGAGTATAGGAGCTTATCTTGTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60
DB 1 GCCTGAGTATAGGAGCTTATCTTGTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60
OY 61 CAATCCCGTCTAAATATATACCAATCGCTTGATCCCTTGCGAGATTAATGCTTAAC 120
DB 61 CAATCCCGTCTAAATATATACCAATCGCTTGATCCCTTGCGAGATTAATGCTTAAC 111
OY 121 GACTATCCCTT 131
DB 112 GACTATCCCTT 122

RESULT 12

US-09-883-119A-29
Sequence 29, Application US/09883119A
Publication No. US20030104520A1
GENERAL INFORMATION:
APPLICANT: The University of Texas System Board of Regents
TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
FILE REFERENCE: 119927-1050
CURRENT APPLICATION NUMBER: US/09/883,119A
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: 60/212,097
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 107
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: oligonucleotide
US-09-883-119A-29

Query Match 60.9%; Score 79.8; DB 9; Length 107;
Best Local Similarity 96.3%; Pred. No. 4.7e-19;
Matches 103; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

OY 27 GTAATCTATCTAAACGGGGAACCTCTCTAGTAGACAATCCCGTCTAAATT-ATACCAGC 85
DB 1 GTAATCTATCTAAACGGGGAACCTCTCTAGTAGACAATCCCGTCTAAATTGATACCAGC 60
OY 86 ATCGTCTGATGCCCTTGCGAG-ATAAATGCCCTAAGCACTATCCCTT 131
DB 61 ATCGTCTGATGCCCTTGCTTGCAATGAATGCCCTAAGCACTATCCCTT 107

RESULT 13

US-09-883-119A-31
Sequence 31, Application US/09883119A
Publication No. US20030104520A1
GENERAL INFORMATION:
APPLICANT: The University of Texas System Board of Regents
TITLE OF INVENTION: Regulatable, Catalytically Active Nucleic Acids
FILE REFERENCE: 119927-1050
CURRENT APPLICATION NUMBER: US/09/883,119A
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: 60/212,097
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 124
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: oligonucleotide

US-09-883-119A-31

Query Match	59.7%	Score 78.2	DB 9;	length 124;
Best Local Similarity	80.9%	Pred. No. 1.9e-18;		
Matches 106; Conservative	0;	Mismatches 18;	Indels 7;	Gaps 1

1 GCCTGAGTATAGGTACTTATCTGTATCTATCTTAACGGGGACCTCTCTAGAGA 60

Db 1 GCCTGAGTATAGCTGACTTACTTGTATCTATCTAATCGGGGAACCTCTCTAGTAGA 60

61 CAATCCGCTAAATTATACACAGCATGCTTGATGCCCTTGGCAGATAATGCCCTAAC 120

Db 61 CAATCCCGTCTAAATTT-----GAGCATATGCTTCGGCAGAAAGCATAATGCCCTAAC 113

121 GACTATCCCTT 131

[illegible]

RESULT 14
US-09-883

```

; Sequence 19, Application US/09883119A
; Publication No. US20030104520A1

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; GENERAL INFORMATION:
: APPLICANT: The University of Texas System Board of Regents

```

Query Match	Score	DB 9;	Length
Post local similarity	58.0%;	Pred. No.	1.1e-17;
	100.0%;		

	best local similarity	100.00;	Mismatches	0;	Gaps	0;
Matches	76;	Conservative	0;	Indels	0;	

1 GCCTGACGATAAGGTGACTTATCTATCTATCTAAACGGGGAACCTCTCTAGTAGA 60

Db
1 GCCTGAGTATAAGCTGACTTATACCTGTATCTATCTAATAACGGGAACTCTCTAGTAGA 60

61 CAATCCGTGTTAAAT 76

RESULT 15

US-09-883-119A-26
; Sequence 26, Application US/09883119A

; Publication No. US20030104520A1
; GENERAL INFORMATION:

OTHER INFORMATION: oligonucleotide
US-09-883-119A-26

Query Match	37.9%	Score 49.6;	DB 9;	length 144;
Best Local Similarity	92.9%	Pred. No. 4.1e-08;		
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4 TGAGTATAAGGTGACTTATACTTGTATCTATCTAAACGGGGAACCTCTCTAGTAG 55

Db

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Search completed: July 13, 2003, 22:56:46
Job time : 106 secs

